

In the Specification:

Please replace the sentences beginning on page 24, line 19 with the following rewritten sentences:

For each contig, more than two genetic markers, developed from the database of BAC-end sequences (http://www.tigr.org/tdb/at/abe/bac_end_search.html) were scored. PCR primers corresponding to these sequences were used to identify size or restriction site polymorphisms in the Columbia and Landsberg ecotypes (Bell and Ecker, 1994; Konieczny and Ausubel, 1993); primer sequences are available (~~<http://genome-www.stanford.edu/Arabidopsis/aboutcaps.html>~~). Tetratype tetrads resulting from treatments that stimulate crossing over (boxes); positions of markers in centimorgans (cM) shared with the recombinant inbred (RI) map (ovals) (~~http://nasc.nott.ac.uk/new_ri_map.html~~; Somerville and Somerville, 1999); and sequences bordering gaps in the physical map that correspond to 180 bp repeats (open circles) (Round *et al.*, 1997), 5S rDNA (black circles) or 160 bp repeats (gray circles) are indicated (Copenhaver *et al.*, 1999).

Please replace the sentence beginning on page 25, line 18 with the following rewritten sentence:

Column 5 notes if the marker is available on public web sites (e.g., ~~<http://genome-www.stanford.edu/Arabidopsis>~~). For those markers that are not available on public web sites the sequences of the forward and reverse primers used to amplify the marker are listed in columns 6 and 7, respectively.

Please replace the sentence beginning on page 28, line 12 with the following rewritten sentence:

Positions in cM on the RI map (~~http://nasc.nott.ac.uk/new_ri_map.html~~) and physical distances in Mb, beginning at the northern telomere and at the centromeric gap, are shown.

Please replace the sentence beginning on page 28, line 17 with the following rewritten sentence:

A single crossover within *CEN4* in the RI mapping population (~~http://nasc.nott.ac.uk/new_ri_map.html~~; Somerville and Somerville, 1999) may reflect a

difference between male meiotic recombination monitored here and recombination in female meiosis.

Please replace the sentence beginning on page 29, line 10 with the following rewritten sentence:

Dashed lines indicate regions in which sequencing or annotation is in progress, annotation was obtained from GenBank records (<http://www.ncbi.nlm.nih.gov/Entrez/nucleotide.html>), from the AGAD database (<http://www.tigr.org/tdb/at/agad/>), and by BLAST comparisons to the database of repetitive *Arabidopsis* sequences (<http://nucleus.cshl.org/protarab/AtRepBase.html>); though updates to annotation records may change individual entries, the overall structure of the region will not be significantly altered.

Please replace the sentence beginning on page 30, line 19 with the following rewritten sentence:

Repeats AtCCS1 (*A. thaliana* centromere conserved sequence) and AtCCS2 (closed and open circles, respectively), AtCCS3 (triangles), and AtCCS4-7 (4-7, respectively) are indicated (GenBank Accession numbers AF204874 to AF204880), and were identified using BLAST 2.0 (<http://blast.wustl.edu>).

Please replace the sentence beginning on page 38, line 2 with the following rewritten sentence:

A dense RFLP map (Chang *et al.*, 1988) and PCR-based maps (Konieczny *et al.*, 1993; Bell *et al.*, 1994) have been generated in *Arabidopsis* from crosses of the Landsberg and Columbia strains (*Arabidopsis* map and genetic marker data is available from the internet at <http://genome-www.stanford.edu/Arabidopsis> and http://cbil.humgen.upenn.edu/atgc/sslp_info/sslp.html).

Please replace the sentence beginning on page 39, line 25 with the following rewritten sentence:

The virtually complete and annotated sequence of chromosomes II and IV was used to conduct an analysis of centromeres at the nucleotide level (<http://www.ncbi.nlm.nih.gov/Entrez/nucleotide.html>).

Please replace the sentence beginning on page 90, line 1 with the following rewritten sentence:

*Adapted from: http://epunix.biols.susx.ac.uk/Home/Neil_Crickmore/Bt/index.html

Please replace the sentence beginning on page 118, line 1 with the following rewritten sentence:

The virtually complete and annotated sequence of chromosomes II and IV was used to conduct an analysis of centromeres at the nucleotide level (<http://www.ncbi.nlm.nih.gov/Entrez/nucleotide.html>).

Please replace the sentence beginning on page 122, line 7 with the following rewritten sentence:

In genetic units, the centromere intervals averaged 0.44 cM, (% recombination = 1/2 tetatype frequency), reflecting recombination rates at least 10-30 fold below the genomic average of 221 kb/cM (Somerville and Somerville, 1999; http://nasc.nott.ac.uk/new_ri_map.html).

Please replace the sentence beginning on page 124, line 9 with the following rewritten sentence:

Annotation of chromosome II and IV (<http://www.ncbi.nlm.nih.gov/Entrez/nucleotide.html>) identified many genes within and adjacent to *CEN2* and *CEN4* (FIG. 8, FIGs. 12A-12T).

Please replace the sentence beginning on page 124, line 21 with the following rewritten sentence:

Within the sequenced portions of *CEN2* and *CEN4*, 17% (27/160) of the predicted genes shared >95% identity with cloned cDNAs (ESTs), with three-fold more matches in *CEN4* than in *CEN2* (<http://www.tigr.org/tdb/at/agad/>).

Please replace the sentence beginning on page 129, line 13 with the following rewritten sentence:

After masking simple repetitive sequences, including homopolymer tracts and microsatellites, contigs of unique sequence measuring 417 kb and 851 kb for *CEN2* and *CEN4*, respectively, were compared with BLAST (<http://blast.wustl.edu>).

Please replace the sentence beginning on page 131, line 21 with the following rewritten sentence:

The following sequenced (<http://www.ncbi.nlm.nih.gov/Entrez/nucleotide.html>) BAC (bacterial artificial chromosome) clones are known to span the region between the markers F5J15-sp6 and T15D9: T13E11, F27C21, F9A16, T5M2, T17H1, T18C6, T5E7, T12J2, F27B22, T6C20, T14C8, F7B19, and T15D9.

Please replace the sentence beginning on page 132, line 11 with the following rewritten sentence:

The following sequenced (<http://www.ncbi.nlm.nih.gov/Entrez/nucleotide.html>) BAC (bacterial artificial chromosome) clones are known to span the region between the markers F5J15-sp6 and T6A13-sp6: T27D20, T19B17, T26N6, F4H6, T19J18, T4B21, T1J1, T32N4, C17L7, C6L9, F6H8, F2I12, F14G16, and F28D6.

Please replace the sentence beginning on page 132, line 27 with the following rewritten sentence:

Genetic positions (*i.e.* cM values) correspond to the Lister and Dean Recombinant Inbred Genetic map, available on-line at http://nasc.nott.ac.uk/new_ri_map.html. Markers are available at <http://genome-www.stanford.edu/Arabidopsis/aboutcaps.html>.

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Please replace the sentence in the table on page 151, line 28 with the following rewritten sentence:

entire chromosome IV	http://websvr.mips.biochem.mpg.de/proj/thal/chr4_announcement/	Dec 17, 1999	
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